



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/806 703
Source: PCT
Date Processed by STIC: 08/30/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER
VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND
TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST 25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be downloaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

<u>ERROR DETECTED</u>	<u>SUGGESTED CORRECTION</u>	SERIAL NUMBER: <u>19/806703</u>
ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE		
1 <input type="checkbox"/> Wrapped Nucleics <input type="checkbox"/> Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping".	
2 <input type="checkbox"/> Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.	
3 <input type="checkbox"/> Misaligned Amino Numbering	The numbering under each 5 th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.	
4 <input type="checkbox"/> Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.	
5 <input type="checkbox"/> Variable Length	Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.	
6 <input type="checkbox"/> PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.	
7 <input type="checkbox"/> Skipped Sequences (OLD RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.	
8 <input type="checkbox"/> Skipped Sequences (NEW RULES)	Sequence(s) _____ missing. If Intentional, please insert the following lines for each skipped sequence: <210> sequence id number <400> sequence id number 000	
9 <input checked="" type="checkbox"/> Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.	
10 <input type="checkbox"/> Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence	
11 <input type="checkbox"/> Use of <220>	Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)	
12 <input type="checkbox"/> PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.	
13 <input type="checkbox"/> Misuse of n	n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.	

AMC/MH - Biotechnology Systems Branch - 08/21/2001

W/1
The type of errors shown exist throughout
the Sequence Listing. Please check subsequent
sequences for similar errors

PCT09

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/806,703

DATE: 08/30/2001
 TIME: 09:49:05

Input Set : A:\3631-109P.ST25.txt
 Output Set: N:\CRF3\08302001\I806703.raw

3 <110> APPLICANT: Steinaa, Lucilla
 4 Mouritsen, Soren
 5 Gautam, Anand
 6 Dalum, Iben
 7 Haaning, Jesper
 8 Leach, Dana
 9 Nielsen, Klaus
 10 Karlsson, Gunilla
 11 Rasmussen, Peter
 13 <120> TITLE OF INVENTION: Novel Methods for Therapeutic Vaccination
 15 <130> FILE REFERENCE: 3631-109P
 17 <140> CURRENT APPLICATION NUMBER: US 09/806,703
 18 <141> CURRENT FILING DATE: 2001-04-04
 20 <150> PRIOR APPLICATION NUMBER: PCT/DK99/00525
 21 <151> PRIOR FILING DATE: 1999-10-05
 23 <150> PRIOR APPLICATION NUMBER: DK 1998 01261
 24 <151> PRIOR FILING DATE: 1998-10-05
 26 <150> PRIOR APPLICATION NUMBER: DK 60/105,011
 27 <151> PRIOR FILING DATE: 1998-10-20
 29 <160> NUMBER OF SEQ ID NOS: 33
 31 <170> SOFTWARE: PatentIn version 3.0
 33 <210> SEQ ID NO: 1
 34 <211> LENGTH: 2253
 35 <212> TYPE: DNA
 36 <213> ORGANISM: Homo sapiens
 38 <220> FEATURE:
 39 <221> NAME/KEY: CDS
 40 <222> LOCATION: (1)..(2253)
 42 <220> FEATURE:
 43 <221> NAME/KEY: misc_feature
 44 <222> LOCATION: (58)..(2253)
 45 <223> OTHER INFORMATION: Human PSM'
 48 <400> SEQUENCE: 1

49 atg kgk aat ctc ctt cac gaa acc gac tcg gct gtg gcc acc gcg cgc 48
 50 Met Xaa Asn Leu Leu His Glu Thr Asp Ser Ala Val Ala Thr Ala Arg
 51 1 5 10 15
 53 cgc ccg cgc tgg ctg tgc gct ggg gcg ctg gtg ctg gcg ggt ggc ttc 96
 54 Arg Pro Arg Trp Leu Cys Ala Gly Ala Leu Val Leu Ala Gly Gly Phe
 55 20 25 30
 57 ttt ctc ctc ggc ttc ctc ttc ggg tgg ttt ata aaa tcc tcc aat gaa 144
 58 Phe Leu Leu Gly Phe Leu Phe Gly Trp Phe Ile Lys Ser Ser Asn Glu
 59 35 40 45
 61 gct act aac att act cca aag cat aat atg aaa gca ttt ttg gat gaa 192
 62 Ala Thr Asn Ile Thr Pro Lys His Asn Met Lys Ala Phe Leu Asp Glu
 63 50 55 60
 65 ttg aaa gct gag aac atc aag aag ttc tta tat aat ttt aca cag ata 240
 66 Leu Lys Ala Glu Asn Ile Lys Lys Phe Leu Tyr Asn Phe Thr Gln Ile

See page 4 of 7

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PATENT APPLICATION: US/09/806,703

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Input Set : A:\3631-109P.ST25.txt
Output Set: N:\CRF3\08302001\I806703.raw

67	65	70	75	80	
69	cca cat tta gca gga aca gaa caa aac ttt cag ctt gca aag caa att				288
70	Pro His Leu Ala Gly Thr Glu Gln Asn Phe Gln Leu Ala Lys Gln Ile				
71	85	90	95		
73	caa tcc cag tgg aaa gaa ttt ggc ctg gat tct gtt gag cta gca cat				336
74	Gln Ser Gln Trp Lys Glu Phe Gly Leu Asp Ser Val Glu Leu Ala His				
75	100	105	110		
77	tat gat gtc ctg ttg tcc tac cca aat aag act cat ccc aac tac atc				384
78	Tyr Asp Val Leu Leu Ser Tyr Pro Asn Lys Thr His Pro Asn Tyr Ile				
79	115	120	125		
81	tca ata att aat gaa gat gga aat gag att ttc aac aca tca tta ttt				432
82	Ser Ile Ile Asn Glu Asp Gly Asn Glu Ile Phe Asn Thr Ser Leu Phe				
83	130	135	140		
85	gaa cca cct cct cca gga tat gaa aat gtt tcg gat att gta cca cct				480
86	Glu Pro Pro Pro Gly Tyr Glu Asn Val Ser Asp Ile Val Pro Pro				
87	145	150	155	160	
89	ttc agt gct ttc tct cct caa gga atg cca gag ggc gat cta gtg tat				528
90	Phe Ser Ala Phe Ser Pro Gln Gly Met Pro Glu Gly Asp Leu Val Tyr				
91	165	170	175		
93	gtt aac tat gca cga act gaa gac ttc ttt aaa ttg gaa cgg gac atg				576
94	Val Asn Tyr Ala Arg Thr Glu Asp Phe Phe Lys Leu Glu Arg Asp Met				
95	180	185	190		
97	aaa atc aat tgc tct ggg aaa att gta att gcc aga tat ggg aaa gtt				624
98	Lys Ile Asn Cys Ser Gly Lys Ile Val Ile Ala Arg Tyr Gly Lys Val				
99	195	200	205		
101	ttc aga gga aat aag gtt aaa aat gcc cag ctg gca ggg gcc aaa gga				672
102	Phe Arg Gly Asn Lys Val Lys Asn Ala Gln Leu Ala Gly Ala Lys Gly				
103	210	215	220		
105	gtc att ctc tac tcc gac cct gct gac tac ttt gct cct ggg gtg aag				720
106	Val Ile Leu Tyr Ser Asp Pro Ala Asp Tyr Phe Ala Pro Gly Val Lys				
107	225	230	235	240	
109	tcc tat cca gat ggt tgg aat ctt cct gga ggt ggt gtc cag cgt gga				768
110	Ser Tyr Pro Asp Gly Trp Asn Leu Pro Gly Gly Val Gln Arg Gly				
111	245	250	255		
113	aat atc cta aat ctg aat ggt gca gga gac cct ctc aca cca ggt tac				816
114	Asn Ile Leu Asn Leu Asn Gly Ala Gly Asp Pro Leu Thr Pro Gly Tyr				
115	260	265	270		
117	cca gca aat gaa tat gct tat agg cgt gga att gca gag gct gtt ggt				864
118	Pro Ala Asn Glu Tyr Ala Tyr Arg Arg Gly Ile Ala Glu Ala Val Gly				
119	275	280	285		
121	ctt cca agt att cct gtt cat cca att gga tac tat gat gca cag aag				912
122	Leu Pro Ser Ile Pro Val His Pro Ile Gly Tyr Tyr Asp Ala Gln Lys				
123	290	295	300		
125	ctc cta gaa aaa atg ggt ggc tca gca cca cca gat agc agc tgg aga				960
126	Leu Leu Glu Lys Met Gly Gly Ser Ala Pro Pro Asp Ser Ser Trp Arg				
127	305	310	315	320	
129	gga agt ctc aaa gtg ccc tac aat gtt gga cct ggc ttt act gga aac				1008
130	Gly Ser Leu Lys Val Pro Tyr Asn Val Gly Pro Gly Phe Thr Gly Asn				
131	325	330	335		

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Input Set : A:\3631-109P.ST25.txt
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133	ttt	tct	aca	caa	aaa	gtc	aag	atg	cac	atc	cac	tct	acc	aat	gaa	gtg	1056
134	Phe	Ser	Thr	Gln	Lys	Val	Lys	Met	His	Ile	His	Ser	Thr	Asn	Glu	Val	
135				340				345						350			
137	aca	aga	att	tac	aat	gtg	ata	ggt	act	ctc	aga	gga	gca	gtg	gaa	cca	1104
138	Thr	Arg	Ile	Tyr	Asn	Val	Ile	Gly	Thr	Leu	Arg	Gly	Ala	Val	Glu	Pro	
139				355				360						365			
141	gac	aga	tat	gtc	att	ctg	gga	ggt	cac	cg	gac	tca	tgg	gtg	ttt	ggt	1152
142	Asp	Arg	Tyr	Val	Ile	Leu	Gly	Gly	His	Arg	Asp	Ser	Trp	Val	Phe	Gly	
143				370				375						380			
145	ggt	att	gac	cct	cag	agt	gga	gca	gct	gtt	gtt	cat	gaa	att	gtg	agg	1200
146	Gly	Ile	Asp	Pro	Gln	Ser	Gly	Ala	Ala	Val	Val	His	Glu	Ile	Val	Arg	
147		385				390						395			400		
149	agc	ttt	gga	aca	ctg	aaa	aag	gaa	ggg	tgg	aga	cct	aga	aga	aca	att	1248
150	Ser	Phe	Gly	Thr	Leu	Lys	Lys	Glu	Gly	Trp	Arg	Pro	Arg	Arg	Thr	Ile	
151					405						410			415			
153	ttg	ttt	gca	agc	tgg	gat	gca	gaa	ttt	ggt	ctt	ctt	ggt	tct	act	1296	
154	Leu	Phe	Ala	Ser	Trp	Asp	Ala	Glu	Glu	Phe	Gly	Leu	Leu	Gly	Ser	Thr	
155					420					425			430				
157	gag	tgg	gca	gag	gag	aat	tca	aga	ctc	ctt	caa	gag	cgt	ggc	gtg	gct	1344
158	Glu	Trp	Ala	Glu	Glu	Asn	Ser	Arg	Leu	Leu	Gln	Glu	Arg	Gly	Val	Ala	
159					435				440			445					
161	tat	att	aat	gct	gac	tca	tct	ata	gaa	gga	aac	tac	act	ctg	aga	gtt	1392
162	Tyr	Ile	Asn	Ala	Asp	Ser	Ser	Ile	Glu	Gly	Asn	Tyr	Thr	Leu	Arg	Val	
163					450				455			460					
165	gat	tgt	aca	ccg	ctg	atg	tac	agc	ttg	gta	cac	aac	cta	aca	aaa	gag	1440
166	Asp	Cys	Thr	Pro	Leu	Met	Tyr	Ser	Leu	Val	His	Asn	Leu	Thr	Lys	Glu	
167		465				470					475			480			
169	ctg	aaa	agc	cct	gat	gaa	ggc	ttt	gaa	gdc	aaa	tct	ctt	tat	gaa	agt	1488
170	Leu	Lys	Ser	Pro	Asp	Glu	Gly	Phe	Glu	Gly	Lys	Ser	Leu	Tyr	Glu	Ser	
171					485					490			495				
173	tgg	act	aaa	aaa	agt	cct	tcc	cca	gag	ttc	agt	ggc	atg	ccc	agg	ata	1536
174	Trp	Thr	Lys	Lys	Ser	Pro	Ser	Pro	Glu	Phe	Ser	Gly	Met	Pro	Arg	Ile	
175					500				505			510					
177	agc	aaa	ttg	gga	aat	gat	ttt	gag	gtg	ttc	ttc	caa	cga	ctt		1584	
178	Ser	Lys	Leu	Gly	Ser	Gly	Asn	Asp	Phe	Glu	Val	Phe	Phe	Gln	Arg	Leu	
179					515				520			525					
181	gga	att	gct	tca	ggc	aga	gca	cg	tat	act	aaa	aat	tgg	gaa	aca	aac	1632
182	Gly	Ile	Ala	Ser	Gly	Arg	Ala	Arg	Tyr	Thr	Lys	Asn	Trp	Glu	Thr	Asn	
183					530				535			540					
185	aaa	ttc	agc	ggc	tat	cca	ctg	tat	cac	agt	gtc	tat	gaa	aca	tat	gag	1680
186	Lys	Phe	Ser	Gly	Tyr	Pro	Leu	Tyr	His	Ser	Val	Tyr	Glu	Thr	Tyr	Glu	
187		545				550					555			560			
189	ttg	gtg	gaa	aag	ttt	tat	gat	cca	atg	ttt	aaa	tat	cac	ctc	act	gtg	1728
190	Leu	Val	Glu	Lys	Phe	Tyr	Asp	Pro	Met	Phe	Lys	Tyr	His	Leu	Thr	Val	
191					565				570			575					
193	gcc	cag	gtt	cga	gga	ggg	atg	gtg	ttt	gag	cta	gcc	aat	tcc	ata	gtg	1776
194	Ala	Gln	Val	Arg	Gly	Gly	Met	Val	Phe	Glu	Leu	Ala	Asn	Ser	Ile	Val	
195					580				585			590					
197	ctc	cct	ttt	gat	tgt	cga	gat	tat	gct	gta	gtt	tta	aga	aag	tat	gct	1824

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198	Leu	Pro	Phe	Asp	Cys	Arg	Asp	Tyr	Ala	Val	Val	Leu	Arg	Lys	Tyr	Ala	
199	595								600			605					
201	gac	aaa	atc	tac	agt	att	tct	atg	aaa	cat	cca	cag	gaa	atg	aag	aca	
202	Asp	Lys	Ile	Tyr	Ser	Ile	Ser	Met	Lys	His	Pro	Gln	Glu	Met	Lys	Thr	
203	610							615			620						
205	tac	agt	gta	tca	ttt	gat	tca	ctt	ttt	tct	gca	gta	aag	aat	ttt	aca	
206	Tyr	Ser	Val	Ser	Phe	Asp	Ser	Leu	Phe	Ser	Ala	Val	Lys	Asn	Phe	Thr	
207	625				630			635			640						
209	gaa	att	gct	tcc	aag	ttc	agt	gag	aga	ctc	cag	gac	ttt	gac	aaa	agc	
210	Glu	Ile	Ala	Ser	Lys	Phe	Ser	Glu	Arg	Leu	Gln	Asp	Phe	Asp	Lys	Ser	
211	645				650			655									
213	aac	cca	ata	gta	tta	aga	atg	atg	aat	gat	caa	ctc	atg	ttt	ctg	gaa	
214	Asn	Pro	Ile	Val	Leu	Arg	Met	Met	Asn	Asp	Gln	Leu	Met	Phe	Leu	Glu	
215	660				665			670									
217	aga	gca	ttt	att	gat	cca	tta	ggg	tta	cca	gac	agg	cct	ttt	tat	agg	
218	Arg	Ala	Phe	Ile	Asp	Pro	Leu	Gly	Leu	Pro	Asp	Arg	Pro	Phe	Tyr	Arg	
219	675				680			685									
221	cat	gtc	atc	tat	gct	cca	agc	agc	cac	aac	aag	tat	gca	ggg	gag	tca	
222	His	Val	Ile	Tyr	Ala	Pro	Ser	Ser	His	Asn	Lys	Tyr	Ala	Gly	Glu	Ser	
223	690				695			700									
225	ttc	cca	gga	att	tat	gat	gct	ctg	ttt	gat	att	gaa	agc	aaa	gtg	gac	
226	Phe	Pro	Gly	Ile	Tyr	Asp	Ala	Leu	Phe	Asp	Ile	Glu	Ser	Lys	Val	Asp	
227	705				710			715			720						
229	cct	tcc	aag	gcc	tgg	gga	gaa	gtg	aag	aga	cag	att	tat	gtt	gca	gcc	
230	Pro	Ser	Lys	Ala	Trp	Gly	Glu	Val	Lys	Arg	Gln	Ile	Tyr	Val	Ala	Ala	
231	725				730			735									
233	ttc	aca	gtg	cag	gca	gct	gca	gag	act	ttg	agt	gaa	gta	gcc	taa		
234	Phe	Thr	Val	Gln	Ala	Ala	Ala	Glu	Thr	Leu	Ser	Glu	Val	Ala			
235	740				745			750									
238	<210>	SEQ	ID	NO:	2												
239	<211>	LENGTH:	750														
240	<212>	TYPE:	PRT														
241	<213>	ORGANISM:	Homo sapiens														
243	<220>	FEATURE:															
244	<221>	NAME/KEY:	misc_feature														
245	<222>	LOCATION:	(58)..(2253)														
246	<223>	OTHER INFORMATION:	Human PSM'														
248	<400>	SEQUENCE:	2														
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	251	1			5				10			15					
	254	Arg	Pro	Arg	Trp	Leu	Cys	Ala	Gly	Ala	Leu	Val	Leu	Ala	Gly	Gly	Phe
	255				20				25			30					
	258	Phe	Leu	Leu	Gly	Phe	Leu	Phe	Gly	Trp	Phe	Ile	Lys	Ser	Ser	Asn	Glu
	259				35			40			45						
	262	Ala	Thr	Asn	Ile	Thr	Pro	Lys	His	Asn	Met	Lys	Ala	Phe	Leu	Asp	Glu
	263				50			55			60						
	266	Leu	Lys	Ala	Glu	Asn	Ile	Lys	Lys	Phe	Leu	Tyr	Asn	Phe	Thr	Gln	Ile
	267				65			70			75			80			
	270	Pro	His	Leu	Ala	Gly	Thr	Glu	Gln	Asn	Phe	Gln	Leu	Ala	Lys	Gln	Ile

- Erroneous: When unknowns are included in a sequence listing, they must be numerated in fields 221, 222, 223.

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/806,703

DATE: 08/30/2001
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Input Set : A:\3631-109P.ST25.txt
Output Set: N:\CRF3\08302001\I806703.raw

271	85	90	95
274	Gln Ser Gln Trp Lys Glu Phe Gly Leu Asp Ser Val Glu Leu Ala His		
275	100	105	110
278	Tyr Asp Val Leu Leu Ser Tyr Pro Asn Lys Thr His Pro Asn Tyr Ile		
279	115	120	125
282	Ser Ile Ile Asn Glu Asp Gly Asn Glu Ile Phe Asn Thr Ser Leu Phe		
283	130	135	140
286	Glu Pro Pro Pro Gly Tyr Glu Asn Val Ser Asp Ile Val Pro Pro		
287	145	150	155
290	160	165	170
291	Phe Ser Ala Phe Ser Pro Gln Gly Met Pro Glu Gly Asp Leu Val Tyr		
294	175	180	185
295	190	195	200
298	205	210	215
302	Phe Arg Gly Asn Lys Val Lys Asn Ala Gln Leu Ala Gly Ala Lys Gly		
303	220	225	230
306	240	245	250
307	255	260	265
310	Ser Tyr Pro Asp Gly Trp Asn Leu Pro Gly Gly Val Gln Arg Gly		
311	270	275	280
314	285	290	295
315	300	305	310
318	320	325	330
319	335	340	345
322	350	355	360
323	365	370	375
326	380	385	390
327	395	405	410
330	400	410	415
331	430	420	425
334	430	435	440
335	445	450	455
338	460	465	470
339	475	480	
342	Asp Arg Tyr Val Ile Leu Gly Gly His Arg Asp Ser Trp Val Phe Gly		
343	370	375	380
346	Gly Ile Asp Pro Gln Ser Gly Ala Ala Val Val His Glu Ile Val Arg		
347	385	390	395
350	400	405	410
351	415	420	425
354	430	435	440
355	445	450	455
358	460	465	470
359	475	480	
362	Tyr Ile Asn Ala Asp Ser Ser Ile Glu Gly Asn Tyr Thr Leu Arg Val		
363	455	460	
366	Asp Cys Thr Pro Leu Met Tyr Ser Leu Val His Asn Leu Thr Lys Glu		
367	480	485	

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/806,703

DATE: 08/30/2001
TIME: 09:49:06

Input Set : A:\3631-109P.ST25.txt
Output Set: N:\CRF3\08302001\I806703.raw

L:50 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:250 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:2070 M:283 W: Missing Blank Line separator, <220> field identifier
L:2101 M:283 W: Missing Blank Line separator, <220> field identifier
L:2166 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:2166 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:2166 M:283 W: Missing Blank Line separator, <400> field identifier
L:2176 M:283 W: Missing Blank Line separator, <220> field identifier
L:2194 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:2194 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION: